

IN THE CLAIMS:

Please cancel claims 9-13 without prejudice or disclaimer, and amend claims 3-4 as follows:

- 1-2. (Cancelled)
3. (Currently Amended) A method for displaying gene expression data, comprising:
 - calculating a first ratio of gene expression levels of a Sample B and a Sample A for each of a plurality of genes in a first experiment-between-a Sample A and a Sample B;
 - calculating a second ratio of gene expression levels of a Sample C and the Sample A for said each of a plurality of genes in a second experiment-between-the Sample A and a Sample C;
 - obtaining a mediated dataset of gene expression levels for the Samples A, B, C expressed as (b/a, c/A, 1) for said each of a plurality of genes;
 - calculating a first magnitude r of said dataset expressed as $r = \sqrt{(b/a)^2 + (c/A)^2 + 1}$; and
 - displaying marks of a first product of the first ratio and 1/r ~~a constant~~, a second product of the second ratio and the 1/r ~~constant~~, and the 1/r ~~constant~~ on coordinate positions with respect to x-, y- and z-axes on ~~or inside~~ a surface of a sphere;
 - ~~wherein the constant is determined to make the marks viewable.~~
4. (Currently Amended) A method for displaying gene expression data according to claim 3, further comprising: ~~calculating a first magnitude and a second magnitude R of said dataset expressed as $R = \sqrt{(b^2 + c^2 + (a + A)^2)}$ each of the marks; calculating a third ratio of the first magnitude and the second magnitude of each of the marks; and using the third ratio as the constant to display magnitude coordinate positions corresponding to the marks inside the sphere~~ displaying marks of a third product of the first ratio and R/r, a fourth product of the second ratio and the R/r, and the R/r on coordinate positions with respect to x-, y- and z-axes.
5. (Previously Presented) A method for displaying gene expression data according to claim

3, further comprising: performing a clustering analysis on the displayed marks on the sphere; and marking at least one gene group obtained by the clustering analysis as a region on the sphere.

6. (Previously Presented) A method for displaying gene expression data according to claim 4, further comprising: performing a clustering analysis on the displayed magnitude coordinate positions inside the sphere; and marking at least one gene group obtained by the clustering analysis as a region inside the sphere.
7. (Previously Presented) A method for displaying gene expression data according to either one of claims 3, 4 and 11, wherein the expression level data is data in a time series, which is displayed based on respective time points for each gene in conjunction with a direction of changes of the coordinate positions with time in the displaying step.
8. (Previously Presented) A method for displaying gene expression data according to either one of claims 5, 6, and 13, wherein the expression level data is data in a time series, and said region is displayed based on respective time points in conjunction with a direction of changes of said region with time in the displaying step.

9-13. (Cancelled)